

Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

Claims 1-26 (Cancelled).

27. (New) A glyoxysomal malate dehydrogenase which is encoded by a nucleic acid sequence comprising:

- a) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:1, or
- b) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:2, or
- c) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be deduced from the amino acid sequence shown in SEQ ID NO:3 by backtranslating, or
- d) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be deduced by backtranslating the amino acid sequence of a functional equivalent of SEQ ID NO:3, which has at least 66% identity with SEQ ID NO:3.

28. (New) A plant nucleic acid sequence encoding a glyoxysomal malate dehydrogenase comprising:

- a) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:1, or
- b) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:2, or
- c) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be deduced from the amino acid sequence shown in SEQ ID NO:3 by backtranslating, or
- d) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be deduced by backtranslating the amino acid sequence of a functional equivalent of SEQ ID NO:3, which has at least 79% identity with SEQ ID NO:3, or
- e) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be deduced by backtranslating the amino acid sequence of a functional equivalent of SEQ ID NO:3, which has at least 87% identity with SEQ ID NO:3.

29. (New) A polypeptide with the biological activity of a glyoxysomal malate dehydrogenase as target for herbicides, encoded by a nucleic acid molecule according to claim 28.

30. (New) A method for detecting functional analogs of SEQ ID NO:2 comprising
a) generating a probe followed by subsequently screening a genomic library or cDNA library of the species in question, or
b) conducting a computer search for analogous sequences in electronic databases.

31. An expression cassette comprising genetic control sequences in operable linkage with a nucleic acid sequence according to claim 28.

32. (New) A vector comprising an expression cassette according to claim 31.

33. (New) A transgenic organism comprising at least one nucleic acid sequence encoding a polypeptide with the biological activity of a glyoxysomal malate dehydrogenase according to claim 28, an expression cassette according to claim 31 or a vector according to claim 32, selected from among bacteria, yeasts, fungi, animal cells or plant cells.

34. (New) A method for identifying substances with herbicidal activity, comprising the following steps:

i. bringing malate dehydrogenase into contact with one or more test compounds under conditions which permit the test compound(s) to bind to the nucleic acid molecule or to the glyoxysomal malate dehydrogenase, and

ii. detecting whether the test compound binds to the malate dehydrogenase of i),
or

iii. detecting whether the test compound reduces or blocks the enzymatic or biological activity of the malate dehydrogenase of i), or

iv. detecting whether the test compound reduces or blocks the transcription, translation or expression of the malate dehydrogenase of i),

the malate dehydrogenase being encoded by a nucleic acid sequence which comprises

a) a nucleic acid sequence according to claim 28, or

b) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be deduced by backtranslating the amino acid sequence of a functional equivalent of SEQ ID NO:3, which has at least 63% identity with SEQ ID NO:3.

35. (New) A method according to claim 34, wherein the malate dehydrogenase is a glyoxysomal malate dehydrogenase and is encoded by a nucleic acid sequence which comprises

a) a nucleic acid sequence according to claim 28, or
b) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be deduced by backtranslating the amino acid sequence of a functional equivalent of SEQ ID NO:3, which has at least 66% identity with SEQ ID NO:3.

36. (New) A method according to claim 34, wherein a test compound is selected which reduces or blocks the enzymatic or biological activity of the glyoxysomal malate dehydrogenase.

37. (New) A method according to claim 34, wherein
i. either malate dehydrogenase is expressed in a transgenic organism or an organism which naturally contains malate dehydrogenase is grown,
ii. the malate dehydrogenase of step i) is brought into contact with a test compound in the cell digest of the transgenic or nontransgenic organism, in partially purified form or in homogeneously purified form, and
iii. a test compound which reduces or blocks the enzymatic activity of the malate dehydrogenase of step a) is selected.

38. (New) A method according to claim 34, which comprises the following steps:
i. generating a transgenic organism according to claim 33 or a transgenic organism comprising a nucleic acid sequence encoding a malate dehydrogenase comprising a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be deduced by backtranslating the amino acid sequence of a functional equivalent of SEQ ID NO:3, which has at least 63% identity with SEQ ID NO:3,
malate dehydrogenase being overexpressed in the transgenic organism,

- ii. applying a test substance to the transgenic plant of i) and to a nontransgenic plant of the same genotype,
- iii. determining the growth or the viability of the transgenic plant and the nontransgenic plant after application of the test compound, and
- iv. selecting test substances which bring about a reduced growth of the nontransgenic plant in comparison with the growth of the transgenic plant.

39. (New) A method according to claim 38, which is carried out in a plant organism, a cyanobacterium or proteobacterium.

40. (New) A method for identifying substances with growth-regulatory activity, which comprises the following steps:

- i. generating a transgenic plant comprising a nucleic acid sequence encoding a polypeptide with the biological activity of a glyoxysomal malate dehydrogenase comprising
 - a) a nucleic acid sequence according to claim 28, or
 - b) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be deduced by backtranslating the amino acid sequence of a functional equivalent of SEQ ID NO:3 which has at least 63% identity with SEQ ID NO:3, malate dehydrogenase being overexpressed in the transgenic organism,
- ii. applying a test substance to the transgenic plant of i) and to a nontransgenic plant of the same variety,
- iii. determining the growth or the viability of the transgenic plant and the nontransgenic plant after application of the test compound, and
- iv. selecting test substances which bring about a reduced growth of the nontransgenic plant in comparison with the growth of the transgenic plant.

41. (New) A method according to claim 34, wherein the substances are identified in high-throughput screening method.

42. (New) A support comprising one or more of the nucleic acid molecules according to claim 28, one or more expression cassettes according to claim 31, one or more vectors according to claim 32, one or more organisms according to claim 33 or one or more (poly)peptides according to claim 29.

43. (New) A method according to claim 34, wherein the substances are identified in High-Throughput Screening using a support according to claim 42.

44. (New) A compound with herbicidal activity, identified by one of the method of claim 34.

45. (New) A compound with growth-regulatory activity, identified by the method according to claim 40.

46. (New) A method for the preparation of an agrochemical composition, which comprises

- a) identifying a compound with herbicidal activity by the method according to claim 8, and
- b) formulating this compound together with suitable auxiliaries to give crop protection products with herbicidal or growth-regulatory activity.

47. (New) A method for controlling undesired vegetation and/or for regulating the growth of plants, which comprises allowing at least one malate dehydrogenase inhibitor according to claim 44 to act on plants, their environment and/or on seeds.

48. (New) A method for generating nucleic acid sequences which encode malate dehydrogenase which is not inhibited by substances according to claim 44, where the nucleic acid sequence comprises a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be derived by backtranslating the amino acid sequence of a functional equivalent of SEQ ID NO:3 which has at least 63% identity with SEQ ID N0:3;

which comprises the following process steps:

- a) expressing the protein encoded by the nucleic acid sequence according to i) in a heterologous system or in a cell-free system;
- b) performing randomized or directed mutagenesis of the protein by modification of the nucleic acid;
- c) measuring the interaction of the modified gene product with the herbicide;
- d) identifying derivatives of the protein which show less interaction;

- e) assaying the biological activity of the protein after application of the herbicide;
- f) selecting the nucleic acid sequences which have modified biological activity with regard to the herbicide.

49. (New) The method according to claim 48, wherein the sequences selected in accordance with step f) are introduced into an organism.

50. (New) A method for the generation of transgenic plants which are resistant to substances according to claim 44, wherein a nucleic acid sequence encoding a malate dehydrogenase which comprises

- a) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:1, or
- b) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:2, or
- c) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be deduced from the amino acid sequence shown in SEQ ID NO:3 by backtranslating, or
- d) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be deduced by backtranslating the amino acid sequence of a functional equivalent of SEQ ID NO:3, which has at least 79% identity with SEQ ID NO:3, or
- e) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be deduced by backtranslating the amino acid sequence of a functional equivalent of SEQ ID NO:3, which has at least 87% identity with SEQ ID NO:3, or
- f) a functional equivalents of the nucleic acid sequence of SEQ ID NO:3 which has at least 63% identity with SEQ ID NO:3;
is overexpressed in these plants.

51. (New) A transgenic plant generated by a method according to claim 50.